

AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Cancelled)
2. (Currently amended) A process for the enhanced production of pantothenate, comprising culturing a recombinant microorganism selected from the group consisting of *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Streptomyces*, *Salmonella*, *Escherichia*, *Klebsiella*, *Serratia*, *Proteus*, and *Saccharomyces* having
 - (i) a deregulated pantothenate biosynthetic pathway, and
 - (ii) a deregulated methylenetetrahydrofolate (MTF) biosynthetic pathway,under conditions such that pantothenate production is enhanced as compared to a wild-type microorganism, wherein the deregulated pantothenate biosynthetic pathway is achieved by overexpressing at least one gene selected from the group consisting of *panB*, *panC*, *panD*, and *panE1*, and wherein the ~~deregulation of the~~ deregulated MTF biosynthetic pathway is achieved by overexpressing at least one gene selected from the group consisting of *gcv*, *serA*, *serC*, *serB*, *glyA*, *sul*, *fol*, *mtrA*, *pab*, *panB* and *purR* derived from a microorganism of the genus *Bacillus*, *Corynebacterium*, *Lactobacillus*, *Lactococci*, or *Streptomyces*.
3. (Original) The process of claim 2, wherein said microorganism has at least two pantothenate biosynthetic enzymes deregulated.
4. (Original) The process of claim 2, wherein said microorganism has at least three pantothenate biosynthetic enzymes deregulated.
5. (Original) The process of claim 2, wherein said microorganism has at least four pantothenate biosynthetic enzymes deregulated.
6. (Original) The process of claim 5, wherein said microorganism has a deregulated ketopantoate hydroxymethyltransferase, a deregualted ketopantoate reductase, a deregulated pantothenate synthetase and a deregulated aspartate- α -decarboxylase.
7. (Previously presented) The process of claim 2, wherein said microorganism further has a

deregulated isoleucine-valine (*ilv*) biosynthetic pathway.

8. (Original) The process of claim 7, wherein said microorganism has at least two isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.
9. (Original) The process of claim 7, wherein said microorganism has at least three isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.
10. (Original) The process of claim 9, wherein said microorganism has a deregulated acetohydroxyacid synthetase, a deregulated acetohydroxyacid isomeroreductase, and a deregulated dihydroxyacid dehydratase.
11. (Previously presented) The process of claim 2, wherein the microorganism has at least one MTF biosynthetic enzyme deregulated.
12. (Original) The process of claim 11, wherein the microorganism has a deregulated *glyA* gene.
13. (Original) The process of claim 11, wherein the microorganism has a deregulated *serA* gene.
14. (Original) The process of claim 11, wherein the microorganism has a deregulated *glyA* gene and a deregulated *serA* gene.
15. (Original) The process of claim 12 or 14, wherein the microorganism has a mutated, deleted or disrupted *purR* gene.
- 16-27. (Canceled)
28. (Previously presented) The process of claim 2, wherein said microorganism is cultured under conditions of excess serine.
- 29-30. (Canceled)
31. (Previously presented) The process of claim 2, wherein the microorganism is a Gram positive microorganism.
32. (Previously presented) The process of claim 2, wherein the microorganism belongs to the genus *Bacillus*.

33. (Previously presented) The process of claim 2, wherein the microorganism is *Bacillus subtilis*.
- 34-49. (Canceled)
50. (Previously presented) The process of claim 2, wherein the microorganism overexpresses relative to a wild-type cell at least one methylenetetrahydrofolate (MTF) biosynthetic enzyme encoded by *glyA*, *serA*, *serC*, *serB*, *gcvT*, *gcvPA*, *gcvPB*, or *gcvH*.
51. (Previously presented) The process of claim 15, wherein the microorganism overexpresses the *glyA* gene as a result of a mutation in the *purR* repressor gene.
52. (Previously presented) The process of claim 15, wherein the microorganism further has a deregulated methylenetetrahydrofolate (MTF) biosynthetic enzyme encoded by *glyA*, *serA*, *serC*, *serB*, *gcvT*, *gcvPA*, *gcvPB*, or *gcvH*.
53. (Previously presented) The process of claim 15, wherein the microorganism further has a deregulated pantothenate biosynthetic pathway.
54. (Previously presented) The process of claim 53, wherein said microorganism has at least two pantothenate biosynthetic enzymes deregulated.
55. (Previously presented) The process of claim 53, wherein said microorganism has at least three pantothenate biosynthetic enzymes deregulated.
56. (Previously presented) The process of claim 53, wherein said microorganism has at least four pantothenate biosynthetic enzymes deregulated.
57. (Previously presented) The process of claim 56, wherein said microorganism has a deregulated ketopantoate hydroxymethyltransferase, a deregualted ketopantoate reductase, a deregulated pantothenate synthetase and a deregulated aspartate- α -decarboxylase.
58. (Previously presented) The process of claim 15, wherein said microorganism further has a deregulated isoleucine-valine (*ilv*) biosynthetic pathway.
59. (Previously presented) The process of claim 58, wherein said microorganism has at least two isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.

60. (Previously presented) The process of claim 58, wherein said microorganism has at least three isoleucine-valine (*ilv*) biosynthetic enzymes deregulated.
61. (Previously presented) The process of claim 60, wherein said microorganism has a deregulated acetohydroxyacid acid synthetase, a deregulated acetohydroxyacid isomeroreductase, and a deregulated dihydroxyacid dehydratase.
62. (Previously presented) The process of claim 15, wherein said microorganism is cultured under conditions of excess serine.
63. (Previously presented) The process of claim 15, wherein the microorganism is a Gram positive microorganism.
64. (Previously presented) The process of claim 15, wherein the microorganism belongs to the genus *Bacillus*.
65. (Previously presented) The process of claim 15, wherein the microorganism is *Bacillus subtilis*.